

Tue Jun 26 17:54:16 2001

4x633148.res

perfect matches in Ig V domain
Seq ID No: 18, 12, 13, 8, 5

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 4x633148.res made by spaula on Tue 26 Jun 101 17:53:40-PDT.

Query sequence being compared: US-08-633-148-4 (1-318)
Number of sequences searched: 18
Number of scores above cutoff: 14

Results of the initial comparison of US-08-633-148-4 (1-318) with:
File: us08_633148_mod.pep

100-

N

U

M

B

E

R

Q

F

S

E

Q

U

E

N

C

E

S

SCORE 0

STDEV

1

35

71

106

141

177

212

247

283

318

4

PARAMETERS

Similarity matrix Unitary K-tuple 2
Mismatch penalty 5 Joining penalty 20
Gap penalty 1.00 Window size 318
Gap size penalty 0.26
Cutoff score 0
Randomization group 0

SEARCH STATISTICS

Scores: Mean Median Standard Deviation
27 11 72.45

Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00

Number of residues: 507
Number of sequences searched: 18
Number of scores above cutoff: 18

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

Sequence Name Description Length Score Score Init. Opt.

1. US-08-633-148-4 Sequence 4, Application US 318 318 4.02 0
The list of other best scores is:

Sequence Name	Description	Length	Score	Init. Opt.
2. US-08-633-148-18 Sequence 18, Application	16	16	16	-0.15 0
3. US-08-633-148-12 Sequence 12, Application	15	15	15	-0.17 0
4. US-08-633-148-15 Sequence 15, Application	11	11	11	-0.22 0
5. US-08-633-148-9 Sequence 9, Application US	11	11	11	-0.22 0
6. US-08-633-148-10 Sequence 10, Application	14	14	14	-0.22 0
7. US-08-633-148-17 Sequence 17, Application	10	10	10	-0.23 0
8. US-08-633-148-16 Sequence 16, Application	10	10	10	-0.23 0
9. US-08-633-148-13 Sequence 13, Application	10	10	10	-0.23 0
10. US-08-633-148-11 Sequence 11, Application	10	10	10	-0.23 0
11. US-08-633-148-8 Sequence 8, Application US	10	10	10	-0.23 0
12. US-08-633-148-7 Sequence 7, Application US	10	10	10	-0.23 0
13. US-08-633-148-5 Sequence 5, Application US	11	11	11	-0.23 0
14. US-08-633-148-21 Sequence 21, Application	11	11	11	-0.23 0
15. US-08-633-148-20 Sequence 20, Application	11	11	11	-0.23 0
16. US-08-633-148-6 Sequence 6, Application US	11	11	11	-0.23 0
17. US-08-633-148-14 Sequence 14, Application	9	9	9	-0.25 0
18. US-08-633-148-19 Sequence 19, Application	10	9	9	-0.25 0

1. US-08-633-148-4 (1-318)

US-08-633-148-4 Sequence 4, Application US/08633148

Initial Score = 318 Optimized Score = 318 Significance = 4.02
Residue Identity = 100% Matches = 318 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

X 10 20 30 40 50 60 70
AQNITARIGEPVLKCKGAPKPPORLEKLTGTETAKVLSFGGGGWDVSVARVLPNGSLFPAVGIODE
|||||
AQNITARIGEPVLKCKGAPKPPORLEKLTGTETAKVLSFGGGGWDVSVARVLPNGSLFPAVGIODE
X 10 20 30 40 50 60 70

GIFRCAMNRNGKETKSNRYRVYQIPGKPEIVDSBELTAGVPNKVGTCSGEGYPAAGTILSHWLDGKPLVP
|||||
GIFRCAMNRNGKETKSNRYRVYQIPGKPEIVDSBELTAGVPNKVGTCSGEGYPAAGTILSHWLDGKPLVP
|||||

NEKGVSVKEQTRRHPTGLTLOSELAVTPARGDPRPTSCFSFGLPRHRLATPIQPRVPEVPLEEY
|||||
NEKGVSVKEQTRRHPTGLTLOSELAVTPARGDPRPTSCFSFGLPRHRLATPIQPRVPEVPLEEY
150 160 170 180 190 200 210

QLVVPEGGAVAPGGTTLTCEVPAQPSQIHMMDGVPLPLPSPVLILPEIGPDQGTSCVATHSSHGP
|||||
QLVVPEGGAVAPGGTTLTCEVPAQPSQIHMMDGVPLPLPSPVLILPEIGPDQGTSCVATHSSHGP
220 230 240 250 260 270 280

QESRAVSISIIIEPGEPTAGSVGGSLGT
|||||
QESRAVSISIIIEPGEPTAGSVGGSLGT
290 300 310 X

2. US-08-633-148-4 (1-318)

US-08-633-148-4 Sequence 18, Application US/08633148

Initial Score = 16 Optimized Score = 16 Significance = -0.15
Residue Identity = 100% Matches = 16 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

X 10 20 30 40 50 60
AQNITARIGEPVLKCKGAPKPPORLEKLTGTETAKVLSFGGGGWDVSVARVLPNGSLFPA

|||||
AQNITARIGEPVLVK
X 10 X

3. US-08-633-148-4 (1-318)

US-08-633-148-12 Sequence 12, Application US/08633148

Initial Score = 15 Optimized Score = 15 Significance = -0.17
Residue Identity = 100% Matches = 15 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

X 10 X 20 30 40 50 60
AQNITARIGEPVLVKCKGAPKPPQRLKMLNTRTEAMKVLSPQGGPWSVARVLPNGSLFLP
|||||
AQNITARIGEPVLVK
X 10 X

4. US-08-633-148-4 (1-318)

US-08-633-148-15 Sequence 15, Application US/08633148

Initial Score = 11 Optimized Score = 11 Significance = -0.22
Residue Identity = 100% Matches = 11 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

130 140 150 160 170 180 190
GSPYAGTSLWHLGKPLVPNEKGVSKQTRRHPTGLTQSELMTVPARGDPRPTFSFSPGLPRHRA
|||||
RGDPRPTFS
X 10

200 210 220 230

LRTAPIQPRVPEVPLEEVQLVPEGGAVAGGTTLT

5. US-08-633-148-4 (1-318)

US-08-633-148-9 Sequence 9, Application US/08633148

Initial Score = 11 Optimized Score = 11 Significance = -0.22
Residue Identity = 100% Matches = 11 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

190 200 210 220 230 240 X
SFSPLPRHRLTAPIQPRVPEVPLEEVQLVPEGGAVAGGTTLTCEVPAQSPQIHWKMGVPLPL
|||||
CEVPAQSPQI
X 10

260 270 280 290

PPSPVLILPEIGPDQGTYSVATHSHGQPSRAVSIS

6. US-08-633-148-4 (1-318)

US-08-633-148-10 Sequence 10, Application US/08633148

Initial Score = 11 Optimized Score = 12 Significance = -0.22
Residue Identity = 85% Matches = 12 Mismatches = 2
Gaps = 0 Conservative Substitutions = 0

30 40 50 60 70 80 90
LEMLNTRTEAMKVLSPQGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNNGKETKSNRYRVYQI
|||||
CRAMNNGKETKSN
X 10 X

100 110 120 130 140

PGKPEIVDSASELTAGVPNKVGTQVSEGSYPAGTSLWHLGK

7. US-08-633-148-4 (1-318)

US-08-633-148-17 Sequence 17, Application US/08633148

Initial Score = 10 Optimized Score = 10 Significance = -0.23
Residue Identity = 100% Matches = 10 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

240 250 260 270 280 290 300
TLTCEVPAQSPQIHWKMGVPLPLPPSPVLILPEIGPDQGTYSVATHSHGQPSRAVSISIIIEPGEEG
|||||
SSHGPOESRA
X 10

310

PTAGSVGGSGGLGT

8. US-08-633-148-4 (1-318)

US-08-633-148-16 Sequence 16, Application US/08633148

Initial Score = 10 Optimized Score = 10 Significance = -0.23
Residue Identity = 100% Matches = 10 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

140 150 160 170 180 190 210
GKPLVPNEKGVSKQTRRHPTGLTQSELMTVPARGDPRPTFSFSPGLPRHRLTAPIQPRVPEP
|||||
SPGLPRHRL
X 10

220 230 240

VPLEEVQLVPEGGAVAGGTTLTCEVPAQSPQIHW

9. US-08-633-148-4 (1-318)

US-08-633-148-13 Sequence 13, Application US/08633148

Initial Score = 10 Optimized Score = 10 Significance = -0.23
Residue Identity = 100% Matches = 10 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

10 X 20 X 30 40 50 60 70
AQNITARIGEPVLVKCKGAPKPPQRLKMLNTRTEAMKVLSPQGGPWSVARVLPNGSLFLPAVGIDQDE
|||||
CKGAPKPPQ
X 10

GIF

10. US-08-633-148-4 (1-318)

US-08-633-148-11 Sequence 11, Application US/08633148

Initial Score = 10 Optimized Score = 10 Significance = -0.23
Residue Identity = 100% Matches = 10 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

220 230 240 250 260 270 X 290
VEPEGAVAGGTTLTCEVPAQSPQIHWKMGVPLPLPPSPVLILPEIGPDQGTYSVATHSHGQPS
|||||
GPQDQGTYS
X 10

300 310

RAVSISIIIEPGEEGTAGSVGGSGGLGT

11. US-08-633-148-4 (1-318)

US-08-633-148-8 Sequence 8, Application US/08633148

Initial Score = 10 Optimized Score = 10 Significance = -0.23
Residue Identity = 100% Matches = 10 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

10 20 30 X 50 60 70

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AQNITARIGEPLVLCKGAPKPPORLEWKLNTGRTAWKVLSPQGGPMDSVARVLPNGSLFLPAVGIQDE
|||||
WKLNTGRTEA
X 10

80
GIFRCQAMNRNGKETK

12. US-08-633-148-4 (1-318)
US-08-633-148-7 Sequence 7, Application US/08633148

Initial Score = 10 Optimized Score = 10 Significance = -0.23
Residue Identity = 100% Matches = 10 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

220 230 240 250 260 270 280 290
VEPEGAVAPGTVLTCEVPAQSPQIHWKDKGVLPPLPSPVLILPEIGPDQGTYSVATHSHGQDES
|||||
GPDQGTYS
X 10

300
RAVSISIIPEEGTAGVGGSLGT

13. US-08-633-148-4 (1-318)
US-08-633-148-5 Sequence 5, Application US/08633148

Initial Score = 10 Optimized Score = 10 Significance = -0.23
Residue Identity = 100% Matches = 10 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

10 X 20 X 30 X 40 X 50 X 60 X 70
AQNITARIGEPLVLCKGAPKPPORLEWKLNTGRTAWKVLSPQGGPMDSVARVLPNGSLFLPAVGIQDE
|||||
CKGAPKKPQ
X 10

GIF

14. US-08-633-148-4 (1-318)
US-08-633-148-21 Sequence 21, Application US/08633148

Initial Score = 10 Optimized Score = 10 Significance = -0.23
Residue Identity = 90% Matches = 10 Mismatches = 1
Gaps = 0 Conservative Substitutions = 0

240 250 260 270 280 X 290 X 300
TLTCEVPAQSPQIHWKDKGVLPPLPSPVLILPEIGPDQGTYSVATHSHGQDESRAVSISIERGEEG
|||||
SSHGQESRAC
X 10

310
PRAGSVGGSLGT

15. US-08-633-148-4 (1-318)
US-08-633-148-20 Sequence 20, Application US/08633148

Initial Score = 10 Optimized Score = 10 Significance = -0.23
Residue Identity = 90% Matches = 10 Mismatches = 1
Gaps = 0 Conservative Substitutions = 0

140 150 160 170 180 190 X
DGKPLVPNEKGVSKQTRRRHPETGLFTLOSELMTVPARGDPRPTFSCFSPGLPRHRLRTAPIQPRVWE
|||||
CSPGLPRHRL
X 10

210 220 230 240
PVPLEEVQLVVEPEGAVAPGTVLTCEVPAQSPQIHT

16. US-08-633-148-4 (1-318)
US-08-633-148-6 Sequence 6, Application US/08633148

Initial Score = 10 Optimized Score = 10 Significance = -0.23
Residue Identity = 90% Matches = 10 Mismatches = 1
Gaps = 0 Conservative Substitutions = 0

10 20 30 X 50 60 70
AQNITARIGEPLVLCKGAPKPPORLEWKLNTGRTAWKVLSPQGGPMDSVARVLPNGSLFLPAVGIQDE
|||||
WKLNTGRTEAC
X 10

80
GIFRCQAMNRNGKETKS

17. US-08-633-148-4 (1-318)
US-08-633-148-14 Sequence 14, Application US/08633148

Initial Score = 9 Optimized Score = 9 Significance = -0.25
Residue Identity = 100% Matches = 9 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

110 120 130 140 150 X 160 170
EIVDSASELTAGVPNKVGTVCVSEGSYPAGTLSWHLDGKPLVPNEKGVSKQTRRRHPETGLFTLOSELMTVP
|||||
EQTRRHPE
X X

180 190 200 210
ARGGDPRPTFSCFSPGLPRHRLRTAPIQPRVWEPV

18. US-08-633-148-4 (1-318)
US-08-633-148-19 Sequence 19, Application US/08633148

Initial Score = 9 Optimized Score = 9 Significance = -0.25
Residue Identity = 90% Matches = 9 Mismatches = 1
Gaps = 0 Conservative Substitutions = 0

110 120 130 140 150 X 160 170
PEIVDSASELTAGVPNKVGTVCVSEGSYPAGTLSWHLDGKPLVPNEKGVSKQTRRRHPETGLFTLOSELMTVP
|||||
CEQTRRHPE
X 10

180 190 200 210
PARGDPRPTFSCFSPGLPRHRLRTAPIQPRVWEPV